REMARKS

The Examiner has objected to the disclosure because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant has amended the specification to delete the embedded hyperlink and/or other form of browser-executable code. Substitute paragraphs that reflect the amendments are enclosed.

Applicants submit that no new matter has been added as a result of this amendment.

Applicant submits that, in view of the above, the claims are patentable and are in condition for allowance. A notice of allowance to that effect is respectfully requested.

Respectfully submitted,

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Date

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3

MARKED UP PARAGRAPHS

On page 22, please amend the first paragraph as follows:

Search tools such as the Basic Local Alignment Search Tool ("BLAST") can also be used to identify cDNAs having substantial sequence identity to one or more sequences in a public database. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (located on the world wide web at [http://www.]ncbi.nlm.nih.gov/). The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, Proc. Nat'l. Acad. Sci. USA 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered substantially identical to a reference sequence if the smallest sum probability in a comparison of the cDNA to the reference nucleic acid is less than about 0.001.

On page 22, please amend the second paragraph as follows:

If a cDNA is identified as substantially identical to a known sequence in a public database, it is assigned an identifier which is the name and the accession number of the sequence with which it is substantially identical. In the case of a cDNA which represents the transcript of a human gene, it is also assigned a UniGene number (located on the world wide web at [http://www.]ncbi.nlm.nih.gov/UniGene and August 1996 NCBI News) if one is available. cDNAs which comprise subsequences which have substantial identity to one or more EST sequences in public databases are also assigned an EST number. cDNAs not having substantial identity to a sequence in a public database, are assigned an identifier designating the sequence as unknown and which is correlated in an array database with all available data relating to the sequence (e.g., sequence information, expression pattern, putative open reading frames, and motifs). In one embodiment of the invention, the user is provided with access to the array database when the user obtains the array.

4

On page 22, please amend the third paragraph as follows:

Search tools also include the Basic Local Alignment Search Tool 2 ("BLAST 2") used to align two given sequences and thereby identify regions having substantial sequence identity. Software for performing BLAST 2 analyses is publicly available through the National Center for Biotechnology Information (located on the world wide web at [http://www.]ncbi.nlm.nih.gov/). The BLAST algorithm performs a statistical analysis of the similarity between the two sequences provided (Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide